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1	CCGGTGCCAG	CCCAGGTGCT	CGCGGCCTGG	CTCC ATG GCC	CTGGTCACAG	TGAGCCGTTC
61	GCCCCGGGC	AGCGGCGCCT	CCACGCCCGT	GGGGCCCTGG	GACCAGGCGG	TCCAGCGAAG
121	GAGTCGACTC	CAGCGAAGGC	AGAGCTTTGC	GGTGCTCCGT	GGGGCTGTCC	TGGGACTGCA
181	GGATGGAGGG	GACAATGATG	ATGCAGCAGA	GGCCAGTTCT	GAGCCAACAG	AGAAGGCCCC
241	GAGTGAGGAG	GAGCTCCACG	GGGACCAGAC	AGACTTCGGG	CAAGGATCCC	AGAGTCCCCA
301	GAAGCAGGAG	GAGCAGAGGC	AGCACCTGCA	CCTCATGGTA	CAGCTGCTGA	GGCCGCAGGA
361	TGACATCCGC	CTGGCAGCCC	AGCTGGAGGC	ACCCCGGCCT	CCCCGGCTCC	GCTACCTGCT
421	GGTAGTTTCT	ACACGAGAAG	GAGAAGGTCT	GAGCCAGGAT	GAGACGGTCC	TCCTGGGCGT
481	GGATTTCCCT	GACAGCAGCT	CCCCCAGCTG	CACCCTGGGC	CTGGTCTTGC	CCCTCTGGAG
541	TGACACCCAG	GTGTACTTAG	ATGGAGACGG	GGGCTTCAGC	GTGACGTCTG	GTGGGCAAAG
601	CCGGATCTTC	AAGCCCATCT	CCATCCAGAC	CATGTGGGCC	ACACTCCAGG	TATTGCACCA
661	AGCATGTGAG	GCAGCTCTAG	GCAGCGGCCT	TGTACCGGGT	GGCAGTGCCC	TCACCTGGGC
721	CAGCCACTAC	CAGGAGAGAC	TGAACTCCGA	ACAGAGCTGC	CTCAATGAGT	GGACGGCTAT
781	GGCCGACCTG	GAGTCTCTGC	GGCCTCCCAG	CGCCGAGCCT	GGCGGGTCCT	CAGAACAGGA
841	GCAGATGGAG	CAGGCGATCC	GTGCTGAGCT	GTGGAAAGTG	TTGGATGTCA	GTGACCTGGA
901	GAGTGTCACT	TCCAAAGAGA	TCCGCCAGGC	TCTGGAGCTG	CGCCTGGGGC	TCCCCCTCCA
961	GCAGTACCGT	GACTTCATCG	ACAACCAGAT	GCTGCTGCTG	GTGGCACAGC	GGGACCGAGC
1021	CTCCCGCATC	TTCCCCCACC	TCTACCTGGG	CTCAGAGTGG	AACGCAGCAA	ACCTGGAGGA
1081	GCTGCAGAGG	AACAGGGTCA	CCCACATCTT	GAACATGGCC	CGGGAGATTG	ACAACTTCTA
1141	CCCTGAGCGC	TTCACCTACC	ACAATGTGCG	CCTCTGGGAT	GAGGAGTCGG	CCCAGCTGCT
1201	GCCGCACTGG	AAGGAGACGC	ACCGCTTCAT	TGAGGCTGCA	AGAGCACAGG	GCACCCACGT
1261	GCTGGTCCAC	TGCAAGATGG	GCGTCAGCCG	CTCAGCGGCC	ACAGTGCTGG	CCTATGCCAT
1321	GAAGCAGTAC	GAATGCAGCC	TGGAGCAGGC	CCTGCGCCAC	GTGCAGGAGC	TCCGGCCCAT
1381	CGCCCGCCCC	AACCCTGGCT	TCCTGCGCCA	GCTGCAGATC	TACCAGGGCA	TCCTGACGGC
1441	CAGCCGCCAG	AGCCATGTCT	GGGAGCAGAA	AGTGGGTGGG	GTCTCCCCAG	AGGAGCACCC
1501	AGCCCCTGAA	GTCTCTACAC	CATTCCCACC	TCTTCCGCCA	GAACCTGAGG	GTGGTGGGGA
1561	GGAGAAGGTT	GTAGGCATGG	AAGAGAGCCA	GGCAGCCCCG	AAAGAAGAGC	CTGGGCCACG
1621	GCCACGTATA	AACCTCCGAG	GGGTCATGAG	GTCCATCAGT	CTTCTGGAGC	CCTCCTTGGA
1681	GCTGGAGAGC	ACCTCAGAGA	CCAGTGACAT	GCCAGAGGTC	TTCTCTTCCC	ACGAGTCTTC
	ACATGAAGAG					
1801	GGACAGGGGG	CCTCAGCCTG	CCCTGAAGTC	CCGCCAGTCA	GTGGTTACCC	TCCAGGGCAG
1861	TGCCGTGGTG	GCCAACCGGA	CCCAGGCCTT	CCAGGAGCAG	GAGCAGGGC	AGGGGCAGGG
1921	GCAGGGAGAG	CCCTGCATTT	CCTCTACGCC	CAGGTTCCGG	AAGGTGGTGA	GACAGGCCAG
1981	CGTGCATGAC	AGTGGAGAGG	AGGGCGAGGC	CTGAGCCCTC	ACACATGCCC	ACGCTCCCCT
2041	GACACTGAAG	AGGATCCACA	ACTCCTTGGA	GAAACACCCT	CACGTCTGTT	GCCGCACACA
2101	TTCCTCTCAG	CTCCGCCCCA	TACCCGTCAC	TACAGCCTCA	CCTCCCACCC	CTGTCACTAC
2161	GGCCTCACCT	CCCACCCCTG	TCACTACAGC	CTCACCTCCT	ACAGCCTTAA	GTCCCAGGCC
2221	CATGTCTGCC	TGTCCAAGGG	CTCAAGACTT	TCTAACTGGG	ATGTGGTAGA	GGGACTGAAG
2281	GTACCTTTGG	GGGCAACAGC	ACCCTAGTTT	CATTCTCAAC	TCTAGCCCTG	CACACTCACC
2341	TGTGGCACGG	AATGAAAACA	GAGCTTCCCG	TGCAAAAAGG	GTCACGCCTC	CCACCCCCGC
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09	DGSPLSNSQPSFPVEILPFLYLGCAKOSTNLDVLEEFGIKYILNVTPNLPNLFENAGEFKYKQIPISDHUSQNLSQFFPEAIS DGSPVPSSQPAFPVQILPYLYLGCAKOSTNLDVLGKYGIKYILNVTPNLPNAFEHGGEFTYKQIPISDHUSQNLSQFFPEAIS ATPPPVGLRASFPVQILPNLYLGSARDSANLESLAKLGIRYILNYTPNLPNFFEKNGDFHYKQIPISDHUSQNLSQFFPEAIE	SDPRYPIYDGGGPYEIL PYLYLGSGNUYCNKULNIQNGISYYLMHSNSCPKP-DFICESRFMRYPINDNYCEKLLPHLDKSI SSCSTPLYDGGGPYEIL PYLYLGSCNHSSDLQGLQACGITAYLNYSRSCPNHFEGLFHYKSIPYEDNQHYEISAHFQERI SSCGTPLHDQGGPYEII PFLYLGSRYHASRKDHLDALGITALINYSRNCPNHFEGHYQYKSIPYEDNHKADISSHFNEAT	NVSYRPAYDQGGPVEILPFLYLGSAYHASKCEFLANLHITALLNYSRBLCPANFEGHTUYKCIPVEDNHKADISSUFNERIE DGSGCYSLPSQPCNEVTPRIYYGNASYAQDIPKLQKLGITHYLNAREGRSFHHVNTNANFYKDSGITYLGIKANDIQEFNLSAYFERAD MEGTMMQQRPYLSQOHPSFT1 NSSPAHSPHAPPETTNEVBBETTMWYN HAFFERAD	**************************************	150	VTVTVAYLHQKLNLSHNDAYDIVKHKKSNISPNFNFHGQLLDFERTLGLS VTVTVAYLHQKHU SI NDAYDFUKDKKSNISDNEWEWGOL DEFDT. SI S	TYTVAYLHQKLHLSLNDAYDLVKRKKSNISPNFNFNGQLLDFERSLRLE TIBIAYIHKTHGHSSDDAYRFVKDRRPSISPNFNFI GOII FYFRTIKII	ITICLAYLIQSHRVRLDEAFDFVKQRRGVISPNFSFNGQLLQLETQVLCH ITICLAYLHRTNRVKLDEAFEFVKQRRSIISPNFSFNGQLLQFESQVLAP	TICHATLAKKKYKLEEHFEFYKQRRSIISPNFSFNGQLLQFESQYLAT TICHAYLAKTKQFRLKEAFDYIKQRRSAYSPNFGFNGQLLQYESEILPS	ILVINTENTENTATOVKSHLSIVRUNRE-IGPNOGFLAQLCQLNORLAKE IATVLAYAKKQYECSLEQALRHVQELRPIARPNPGFLRQLQIYQGILTAR ItAYIMslA!krisPNf.F%gQLl#l
50	NVTP NVTP	MHSN NVSR NVSR	NYSR	N.S.	140	TOLVKHKKS	TOL VKRKKSN TRF VKDRRPS	-DFVKQRRGY -EFVKQRRS1	EFVKORRSI DYIKORRSH	SIVRUNKE- RHVQELRPI
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10	PLSNSQPSFP PVPSSQPRFP PPVGLRRSFP PFI PVPSUGI	RVPIYDOGGP STPLYDOGGP GTPLHDOGGP	YRPAYDQGGP GCYSLPSQPCI	.d	100	EA-RGKNCGVI EA-RSKKCGVL	ER-LSQNCGVI (R-KLSSCQV)	ST-KNAGGRUF ST-KNAGGRUF SV-KNEDED:	V-REKGGKVL	AR-RAGGTHVI.
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	PYST1 MKP-7 MKP-4	PRC1 KP-1 KP-2	MKP-5 VHR AK001790	Consensus		PYST1 MKP-7	AKP-4	EKP.1	KP-5	RK001790 Con en us

1 CCGGTGCCAG CCCAGGTGCT CGCGGCCTGG CTCCATGGCC CTGGTCACAG TGAGCCGTTC 61 GCCCCGGGC AGCGGCGCCT CCACGCCCGT GGGGCCCTGG GACCAGGCGG TCCAGCGAAG 121 GAGTCGACTC CAGCGAAGGC AGAGCTTTGC GGTGCTCCGT GGGGCTGTCC TGGGACTGCA 181 GGATGGAGGG GACAATGATG ATGCAGCAGA GGCCAGTTCT GAGCCAACAG AGAAGGCCCC 241 GAGTGAGGAG GAGCTCCACG GGGACCAGAC AGACTTCGGG CAAGGATCCC AGAGTCCCCA 301 GAAGCAGGAG GAGCAGAGGC AGCACCTGCA CCTCATGGTA CAGCTGCTGA GGCCGCAGGA 361 TGACATCCGC CTGGCAGCCC AGCTGGAGGC ACCCCGGCCT CCCCGGCTCC GCTACCTGCT 421 GGTAGTTTCT ACACGAGAAG GAGAAGGTCT GAGCCAGGAT GAGACGGTCC TCCTGGGCGT 481 GGATTTCCCT GACAGCAGCT CCCCCAGCTG CACCCTGGGC CTGGTCTTGC CCCTCTGGAG 541 TGACACCCAG GTGTACTTAG ATGGAGACGG GGGCTTCAGC GTGACGTCTG GTGGGCAAAG 601 CCGGATCTTC AAGCCCATCT CCATCCAGAC CATGTGGGCC ACACTCCAGG TATTGCACCA 661 AGCATGTGAG GCAGCTCTAG GCAGCGGCCT TGTACCGGGT GGCAGTGCCC TCACCTGGGC 721 CAGCCACTAC CAGGAGAGAC TGAACTCCGA ACAGAGCTGC CTCAATGAGT GGACGGCTAT 781 GGCCGACCTG GAGTCTCTGC GGCCTCCCAG CGCCGAGCCT GGCGGGTCCT CAGAACAGGA 841 GCAGATGGAG CAGGCGATCC GTGCTGAGCT GTGGAAAGTG TTGGATGTCA GTGACCTGGA 901 GAGTGTCACT TCCAAAGAGA TCCGCCAGGC TCTGGAGCTG CGCCTGGGGC TCCCCCTCCA 961 GCAGTACCGT GACTTCATCG ACAACCAGAT GCTGCTGCTG GTGGCACAGC GGGACCGAGC 1021 CTCCCGCATC TTCCCCCACC TCTACCTGGG CTCAGAGTGG AACGCAGCAA ACCTGGAGGA 1081 GCTGCAGAGG AACAGGGTCA CCCACATCTT GAACATGGCC CGGGAGATTG ACAACTTCTA 1141 CCCTGAGCGC TTCACCTACC ACAATGTGCG CCTCTGGGAT GAGGAGTCGG CCCAGCTGCT 1201 GCCGCACTGG AAGGAGACGC ACCGCTTCAT TGAGGCTGCA AGAGCACAGG GCACCCACGT 1261 GCTGGTCCAC TGCAAGATGG GCGTCAGCCG CTCAGCGGCC ACAGTGCTGG CCTATGCCAT 1321 GAAGCAGTAC GAATGCAGCC TGGAGCAGGC CCTGCGCCAC GTGCAGGAGC TCCGGCCCAT 1381 CGCCCGCCCC AACCCTGGCT TCCTGCGCCA GCTGCAGATC TACCAGGGCA TCCTGACGGC 1441 CAGAACC<u>TGA</u> GGGTGGTGGG GAGGAGAAGG TTGTAGGCAT GGAAGAGAC CAGGCAGCCC 1501 CGAAAGAAGA GCCTGGGCCA CGGCCACGTA TAAACCTCCG AGGGGTCATG AGGTCCATCA 1561 GTCTTCTGGA GCCCTCCTTG GAGCTGGAGA GCACCTCAGA GACCAGTGAC ATGCCAGAGG 1621 TCTTCTCTTC CCACGAGTCT TCACATGAAG AGCCTCTGCA GCCCTTCCCA CAGCTTGCAA 1681 GGACCAAGGG AGGCCAGCAG GTGGACAGGG GGCCTCAGCC TGCCCTGAAG TCCCGCCAGT 1741 CAGTGGTTAC CCTCCAGGGC AGTGCCGTGG TGGCCAACCG GACCCAGGCC TTCCAGGAGC 1801 AGGAGCAGGG GCAGGGGCAG GGGCAGGGAG AGCCCTGCAT TTCCTCTACG CCCAGGTTCC 1861 GGAAGGTGGT GAGACAGGCC AGCGTGCATG ACAGTGGAGA GGAGGGCGAG GCCTGAGCCC 1921 TCACACATGC CCACGCTCCC CTGACACTGA AGAGGATCCA CAACTCCTTG GAGAAACACC 1981 CTCACGTCTG TTGCCGCACA CATTCCTCTC AGCTCCGCCC CATACCCGTC ACTACAGCCT 2041 CACCTCCCAC CCCTGTCACT ACGGCCTCAC CTCCCACCCC TGTCACTACA GCCTCACCTC 2101 CTACAGCCTT AAGTCCCAGG CCCATGTCTG CCTGTCCAAG GGCTCAAGAC TTTCTAACTG 2161 GGATGTGGTA GAGGGACTGA AGGTACCTTT GGGGGCAACA GCACCCTAGT TTCATTCTCA 2221 ACTCTAGCCC TGCACACTCA CCTGTGGCAC GGAATGAAAA CAGAGCTTCC CGTGCAAAAA 2281 GGGTCACGCC TCCCACCCCC GCCCCCTCCC TGCACCTCCT GTCCTCTCCC AGTTCATTCC 2341 TGGAACCAGC CAGGCCAGGC AACCAGTGGC CCCCAAAGGC AGGCAGGATC CTCAGGCCCC 2401 AGCCGCGGA GGCTGGAAGG GCTGGCAGAT CGCTTCCCTC ATCCACCTCC ACCGGTCCAG 2461 GTCTTTGCTG CTGTCCCCAG ACCTCCTGTG ACACCACGCC AGATCACAGG GCACCAGGCC 2521 AGAGATAGTC TTCTTTTGT CCTTTCTGGC CTCTGGCTAG TCAGTTTTTC ATAGCCTTAC 2581 AGTATCTGGC TTTGTACTGA GAAATAAAAC ACATTTTC

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	131		• 1	• 1	170		180	190	200	200 210		220	230	240	250	260
0SP-15 RB036834 0SP-13 0SP-12 Consensus	VVSTREG AGDNKNT VVSTNGR	VVSTREGEGLSQDETVLLGVOFPDSSSPSCTLGLVLPL RGDNKNTSGMEESCLLGTDCNERTTIGLVVPJ VVSTNGRQDTEESIVLGMOFSSNDSSTCTHGLVLPL MVLRL	VLLGVOFPI CLLGTDCNI IVLGNOFSI 1.1g.d	DSSSPSCT ERTT SNDSSTCT	LGLVLPLHS TGLVVPTLA HGLVLPLHS HVLRLHS .g\$Vlplus	OTTACE OTTACE OTTACE OTTACE OTTACE OTTACE	DGGFSVKI SDGGFSVKI SDGGFSVST SDGGFSVST SDGGFSVSt	GEGSRIF VEKTHIF DNRVHIF GERMHIF	KPISIQIMH KPVSVQRNN KPVSVQRNN KPVSVQRNN	RTLQVLHQ SALQTLHK SALQSLHK SALQVLHK səLQVLHK	RCERRLGS VSKKRREN RCEVRRRH RCEVRRRH RCEVRRRH	MFYRSGPS NYYPGSLF NYFPGGVR NYFPGGVR	LTHISHYO HDMLSSYE LTHVSYYE LIHRTYYE	HSDTQYYLDGDGGFSYTSGGQSRIFKPISIQTMURTLQVLHQRCERRLGSGLYPGGSRLTHNSHYQERLNSEQSCLNEUTRHRADLESLRPPS LHOTTIALDGDGGFSVKYYEKTHIFKPVSVQRHUSRLQTLHKVSKKRRENNFYRSGPSHDALSSYERRIESDGSCLNEUNRHDALESRRPPS HSDTLIALDGDGGFSVSTDNRVHIFKPVSVQRHUSRLQSLHKRCEVRRAHNYPPGSLFITNVSYYESHINSDQSSVNEUNRHQDVQSHRPDS HSDTKTHLDGDRGGFSVSTRGRHHIFKPVSVQRHUSRLQVLHKRCEVRRAHNYPPGGVRLINATYYESCISSEGSCINEUNRHQDLESTRPDS LKSDT.IHLDGDGGFSVst.gr.hIFKP!S!QaMXsaLQvLHKacevRr.hny.pgg.al.NasyY#s.1.S#QSc.NEUNRHQDLESTRPDS	NENTAKBOLE NENNAMBALE NENNAMBALE NENNAMBALE NENNAMBALE	SERPPS SERPPS SERPPS STRPDS STRPDS
	261	270	280	230	300	•	310	320	330	340	(7)	350	360	370	380	330
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	391	400	410	450	430		440	450	460	470	4	480	490	200	510	520
0SP-15 RB036834 0SP-13 0SP-12 Consensus	LLPHYKE LLRYWDD LLAYWDD LLAHWKE LLAHWKE	LLPHUKETHRFIERRRQGTHVLYHCKNGVSRSARTVI LLRYNDDIFRYTTRRKREGSKYLYHCKNGVSRSASVVI LLRYNNDTYKFISKRKHGSKCLYHCKNGVSRSASTVI LLRHWRERYHFINKRKNHSKCLYHCKNGVSRSASTVI LLankn&U&XI.kRkgskcLYHCKNGVSRSRSLVI	RRGGTHVL KREGSKYL KKHGSKCL KRNHSKCL C. gskCL	VHCKMGVS VHCKMGVS VHCKMGVS VHCKMGVS		PRKQYEC PRKRYQU PRKEYGU PRKEFGU PRKEFGU	SLEGALRHY FROGALEHV KLDRAYDYV VLEKAYNYV 1#.Ry.yV	QELRPIA KKRRSCI KERRTVI KQKRSII K.RSIL	AYANKQYECSLEGALRHVQELRPIARPAPGFLRQLQIYQGILTASRQSHVAEQK RYANKEYGUNLDRAYDYVKERRSCIKPAKNFLNQLETYSGALDAHKKEKLQRS RYANKEYGUNLDRAYDYVKERRTVTKPAPSFRQLEEYQGILLASFLGLIHGGR RYANKEFGUPLEKAYNYVKQKRSITRPNAGFNRQLSEYEGILDASKQRHNKLUR AYANKAXQU.1#.Ay.9VkRsitrPN.gF\$FQL.eY.GildAskq.h	LOTYGGIL LETYSGAL LEEYGGIL LSEYEGIL L. 07. GIL	TRSRQSHV ORMKNEK LASFLGLI ORSKQRHN ORSKQRHN	HEGKVGGV LGRSKSET HGGRDKPK KLURGQTD	SPEEHPRP NLKSTKOR GEKSTEFE SSLQQPVO 5P	AYARKQYECSLEGALRHYQELRPIARPNDGFLRQLQIYQGILTASRQSHYNEQKYGGYSPEEHPAPEVSTPFPPLPPEGGGEEKYVGKE FRYRKRYQWEFQQRLEHYKRRSCIKPNKKFLNQLETYSGALDAKKKKLQRSKSETNLKSTKORRLLPGSEPTPLI-QAKSKSTGE FRYRKEYGWHLDRAYDYVKERRTVIKPNPSFHRQLEEYQGILLASFLGLIHGGROKPWGEKSTEFESYDLVSIPGSPSCCNPEKLLHISH FRYRKEFGWPLEKAYNYVKQKRSITRPNAGFHRQLSEYEGILDASKQRHNKLARQQTDSSLQQPVODPAGPGDFLPETPDGTPESQL	PEPEGGEEKY LI-GRLNGRKS GSPSCCNPEKL ETPDGTPESQL	SKSTGE CLHISH
	521	530	540	550	560		570	280	530	900	9	610	620	630	640	650
0SP-15 RB036834	SQRAPKEE RGVTPDGE	EPGPRPRII EEEDGSRNI	NL RGVKRS. IRRSIROK	ISLLEPSL SQRRHV	ELESTSETS RRSSSTSPK	DHPEVFS: TQTRVVTI	SHESSHEEP COOSOSHER	LAPFPAL	ART-KGGQQ HEEPKNMRF	VORGPOPA	KSRQSVV	TLOGSAVV Hiokhtpl	RINKTORFO SVRTRIHD	SQARPKEEPGPRPRINLRGYMRSISLLEPSLELESTSETSOMPEVFSSHESSHEEPLQPFPQLART-KGGQQVDRGPQPALKSRQSVYTLQGSRVYANRTQAFGEQEQGGGEPCISSTPRFKVVR RGYTPDGEEEDGSRHARRSIAQKSQRRHVRRSSSTSPKTQTRVYTKQQSQSHENLTPERSYAEEPKHMRFPGSHGENYSYTQNQVLHIQKHTPLSVRTRIHDLERHRADQLPQQPVHTSLTKLITQTS	GEPCISSTPR QQPVHTSLTX	FRKVVR LITQTS
DSP-12 Consensus	PFL00AB	PFLDDBRQPGLGPPLPCCFRRLSDPLLPSI P-J-PP8-8P	PCCF	RRLS		EDEAGSL VHL	EDPERERLL	LEERRPPI	1EVHRPARQI 3erq	PQQGSG	LCEKDVKK	KLEFGSPK 1P.	GRSGSLLQ	'EDEAGSLYHLEDPEREALLEEAAPPAEVHRPARQPQQGSGLCEKDVKKKLEFGSPKGRSGSLLQVEETEREEGLGAGRUGQLP-	GAGRAGQLP- 84.1p.	1
	651	099	670	089	069		200	710	720	730	7	740 746				
0SP-15 88036834	QASVADSGEEGER Hlgksvsgsssgn	ARSVADSGEEGER Hlgksvsgsssgnidsradsscsdyfssqvdsyfakde	SRROSSCSI	OVFSSQVD		KRQRRKTI	1SWTESLGP	SGGIVLD	GEKRQRRKTHSUTESL GPSGGIVLOPTPQQQKQQSNRILRPRGTRQRELPSRHRSUGS	SNRILRPR	STRQREL P	SRHASAGS				
DSP-12 Consensus	QLDQNLL ql	QLDQNLLNSENLNNNSKRSCPNGNEVGRARPA 91sen.sspr.ssc	SKRSCPI	NGE		PSLP		TSRSVVG	-WAPTSASYVGTTGTRHHTQLIFFYCLLWAPSSHLQGPEGSFTG	LIFFYCLL	ARPSSHLQ	GPEGSFTG				